

090303E 0001

1	AAGCTTTCTTGGCCCCCTAACAGCAACCACATTATACTCTTACTGGCTATTCTCTTGGCCTT	60
61	CAATACCCAGCCCAGGGGACCCCTCTTCCAGGGAGCCCCGCTTGTACTCCTGAGATGTCA	120
121	TGTCCTTCTTGCAGAGCTCTTCCTCACGGCATCGGGACGGCGGTTACCCCTTTTGCCTCT	180
181	CCGGATAAACTGTAAGCTACTTGAGAGCAGAGAACATCCATTGTTTCGCTGTGGCATCCGT	240
241	GGTACCTAGCACGGCATCTGACATATTATCAGATCTTCCACAAAGGCCAGTTTACGGTTG	300
301	AATGCCCCGTTGAATTCAAGGCTCCCAGTGGGAGAGCGAGGAAGTAATAAAGCCGGTGATAA	360
361	ATGCCGCCGTGGAGACACCAGCGGGCTGCCGTGAGACTAATGGAGAGGACAGTAACGTTA	420
421	TCTCTAATGCGAGGGTGGTTATAGAGTACATTTTCATAACACCTTTAAAGCTCTTTCACAC	480
481	GCATTATCCAATTTGATCCTCATAAAAGCCTGGAGATGTGTATATTGTGGTGGATGGAGG	540
541	GGGAGTCTTTAGCAGTTATGGGATATGCCTGAAGTCGTGCAGCTAGTAAATGGCTGGATT	600
601	CAAACCAGACCTCAAAGCCTGCCTGTTTGCTCATGCCCCCTGCCCGACTGCCCACTCT	660
661	GTGGCCACAGCACAACTCACCGTCGCTTTCTTGATCCGTTTTCTTGATCCGGCTGTGCT	720
721	CTCCCCAAGGAATGCTTTTCATTAACATATGTCTAGGTAATGAATTATCTTGACTCTGAG	780
781	GAGGCCATAGCACATGCCGTAACGCGACAGCTCCTTTGATCTGCATCTGAGGCTGTGGCT	840
841	GGTAACGGGCGTGGGGAGGGGGCGTTCGCTGAGACCCAGGGACACGCCATGTGTGGTTC	900
901	CCTCTGTTTCCAGGCCCCAGAAGCACATCCCGGAAAGGAAATGCGCTGTGGACCCCTGT	960
	M R C G P L C	
961	GCCGATTCTTGCTGGCTTTGGCCTATCTGTCTACGTTGAAGCCGTGCCCATCTGGAGAG	1020
	R F L L A L A Y L S Y V E A V P I W R V	
1021	TCCAGGATGACACCAAAACCTCATCAAGACGATTGTCAACCAGGATCAGTGACATTTAC	1080
	Q D D T K T L I K T I V T R I S D I S H	
1081	ACATGGTAGGGAAGGCCTGGGAGACAAGGTGGAACCTGTGGCCAGCCCSGGGGGAGGAGG	1140
	M	
1141	GGTACCGGACCTCAGAGGTTGGCGGAGGTGGGAAGGGTCGGCGGTGGCCTTGACGCCTCC	1200
1201	CCCACCCCCCAACCAGCTGCCTTTGCTCCTCCGCTTCCCTCACCGCACCCCCCACGT	1260
1261	CCTTATCCTCCTTCTTCCCAGACTGGAATCCTGATGCCAGGACTAGAGGAAGCCCTAAA	1320
1321	GGTCCTGTGTGCCTTTGCCAGGTGCGCAGACCCCCCAGCATCATCCCTCTGGCCTCCAT	1380
1381	CACGTCTCCGGAATGTTCTAATCTGTAGGAATTCTTCTGGTGACAGCTGAACTCTGACC	1440
1441	CTGCGGACGCCCCCTTACTGCTAGTCCTGCCATTGAGCCTTTTTTCTATACAACCCTCT	1500
1501	ACATGTTTGCAAACCTTCTCTCAATGTCCCCAGGGTGTTTTCTCTGGGGTCCGCAGGCCGA	1560
1561	GACCTTCAGCCTCTTCTCAGCTGAGGTCCGTCTTTAGAATTGAGAAGACGAGGTGTGACT	1620
1621	CCTCACCTGCTGTTCCCTCTCTGTAAATCTCAAGCACGTTAAGTCCCTCCGTGTCTGA	1680
1681	AACCTTAGTTTTCCCTCATCCAGATAATGGGACTGTACTGGGAAGATGTTACCGGAATCC	1740
1741	AGGGTCTTGCTCATGGAGCTCAAGAATGAACTTGGCGAACGCACAGGGAGCCGAGCAAG	1800

FIG. 1B

1801	CAGAAGTCTTTATTACAGGAAGGCAGACAGCTCCCAGCACAGACACGGGGAGGGGAAGAGT	1860
1861	CCCCCGCCCATTTGTTCTACGGAGGTTTTTATCACTTAAAGACGGGAGTACCAATGTGGG	1920
1921	GTCCAGATATCCGTTCTTCTTCCCATTGCCAGTTTACCTATATGGCGCCTTGTCAGGA	1980
1981	GGGACTCTGTAGAGTTAGGGGTGCTCCGTAAGTTTTATGGTGCGTCTGCTCTTCTCTGCC	2040
2041	CTAGACTTAGAGTCGCCACTCTTTCCATTCTTCTGCTCACAGTCAAATGCATAGGTCAGG	2100
2101	GGTTAATTCCACCTTCACAGAAATCAAATGTCCTTTCAATAGTTAATCTTCCAATAAGC	2160
2161	AAGGCCTGCTTGTCTTGATTAGTTTTTACAAATCTTAAACCATGGCCATTAATCAGGGAA	2220
2221	GAGATCGAAGCCCATGTTCCACACTAAGTGCCTGAATTATTAGTCTGCCTCAGGACTAT	2280
2281	CTTAATAGTCTTCGCAAGGTTGTTTTGAGATTAAATTAGATAGGAGTTCCTGTGAGGCG	2340
2341	CGACGGAAACAGATCCGACTCAGAACCATGAGACAGGTTGATCCCTGGCTTTGTCAGTG	2400
2401	GGTTAGGATCTGGTGCTGCTGTGAGCTGTGGTGTAGGTCGCAGAGGTGGCTCGGATCCCG	2460
2461	CGTTGCTGTGGCTGTGGTGTAGGCCGGTGACAGAGCTCCGATTAGACCCCTAGCCTGGG	2520
2521	AACCTCCATGTGCCGCGGGTACCGCTAAAAAAGACAAAAAGATGGAAAAAAGGTTA	2580
2581	CATTAGATAAAGCAAGTGACTCCTCCACCACCACACATATCCCTGCAGAACCAGGACAGA	2640
2641	GCATGCCTTCTTGAAAAGTTTTCGGTTGTGGCTTTGATAGCACCCAGCCTTAAAGCCAG	2700
2701	CTTTTCAATCTGCCCAGAGCAGTCTGGAGACTTCCGCATCTCCTGGCCACTCTGAGTTTC	2760
2761	TAACAGTGGCCTTGGCGAGCCTGGGAGCAGTCCGGTGGCCAGAAGCAGGGACAGCTGAGA	2820
2821	ACCAGATAGAGTCTTGGCACTTTCAAGAGAAAAACCCTAAGTCTCCTTCTTCAGCCATGC	2880
2881	AACAGCTGCGCATGACAGATCCAGCGTGTCCCAGCCTGTGTGGTGCAGGGAGTGAYGCTG	2940
2941	CGNNYAGGGYGYGGGGAGCTGAGGAGCGAGGCGGGGCATCGNGGGGCTGCAGCCTCCAT	3000
3001	CCCTAAGTGGGGAGACTTCATGAAGAGCCTGACCAGNAGGGAGGGGCATGTGTGGAGGAC	3060
3061	CTCAGGGCCTGGGGAAGGCTAGACCCAACTATGTGAGAAACAGACAGTCGTGGCTGGTTC	3120
3121	TACAGAAGAGGCATCTGGAGGCCATTGCAATGCCCAAAGCTGTCTGGGTGAGGCAGGGCT	3180
3181	TGCTAGGCAGAAGACAGAAGGCCGTGAGACCAGCTTGGAGGCTTGGCAGCCACGCCAGCC	3240
3241	CAAGGAGTTCGGGCCTAGATAGGATTGTGTGGAAGGGGAAGAGGCAGCCGAGGTGGGGG	3300
3301	GTGGGGGTGGACCCGTCTCCACGCCTGCAGGAAGGCCAGGGGCTGCAGAGCCAACATCTC	3360
3361	TCTCGCTGAGCGTCTCGCTCTCCCCCTTCTCCTGCACAGCAGTCTGTCTCCTCCAAACAG	3420
	Q S V S S K Q	
3421	AGGGTCACCGGTTTGGACTTCATCCCTGGGCTCCATCCTGTCTGAGTTTGTCCAAGATG	3480
	R V T G L D F I P G L H P V L S L S K M	
3481	GACCAGACCCTGGCGATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATC	3540
	D Q T L A I Y Q Q I L T S L P S R N V I	
3541	CAAATATCGAATGACCTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCTCCAAG	3600
	Q I S N D L E N L R D L L H L L A S S K	
3601	AGCTGCCCCCTTGCCCAGCAGGGCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCTGGAA	3660
	S C P L P S R A L E T L E S L G G V L E	

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FIG. 1C

3661 GCCTCCCTCTACTCCACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGAC 3720  
 A S L Y S T E V V A L S R L Q G A L Q D  
 3721 ATGCTGCGGCAGCTGGACCTCAGCCCTGGCTGCTGAAGCCTTGAAGGCCTCTCTCCCCAC 3780  
 M L R Q L D L S P G C \*  
 3781 AGTCGGGGGAAGAAACCTGAGCTTCCAGGAGTCTGCTGGAGAAGAGAGCCTGTGCGGACC 3840  
 3841 TCCTCTCTGCAGGTCTGCGGACCATTTCTCTCTCGCTCCGCTAAGCTGCTCTTCCAAAGG 3900  
 3901 CAGAAAACCTCAAGGCACGACACCAAAGACAGAAAGGCCTGGTTCGCGCGCCACCGGAAA 3960  
 3961 GGGGGCGCCGTCCAGCCAACGGTGGACTAGATTTTCGGATTTTCCACCAACGTCTTCCTTC 4020  
 4021 CTGTTCCATCTCCAGCTCACCGCGTGCTTCAGCGTGACCGGGGGGATTTTCAGAGCCTTTC 4080  
 4081 GACCATCAAGCAGGGTTCCATCTGAGAATTCCGGGGAGCACGGTGAAGGCTACAGGCACA 4140  
 4141 CACAGCTGGATGCTCCACGCAACACAAGTTGGAAGCATTTCTTTATTTATTATGCGGTG 4200  
 4201 TATTCTGGTTGGATTTGAAGCAAAACACCAGCCTTTCCAGGCTCTCTGGGGTCAGCCGGG 4260  
 4261 GCTAGGGGGAGGCTCCCGAGGTGCTGTTTCCAGTACCATCCATGGGCCTGCTGAGGCCAA 4320  
 4321 CCCATTTTGAGTGACTTGAGGGCTCTCAAGGTCGTTCTCTAGAGACTGGCTTTGTTTCTA 4380  
 4381 CTGTGACTGACTTTAAACTGCAGCGTGTGCACTGGCATCGCCTGCGCGGATCTCGAAGG 4440  
 4441 GCCAGGTTCTCTTAGAAAGAAGAAGATGAACCTTTGTGAGGGGTGTGTACGCGGAGACAGG 4500  
 4501 AAGTGTGTTGGTGGGCGGGGCATGGATCCAGAATGTGTATTTCTTGTGTGATGGACATTT 4560  
 4561 GTGTGAGGGGCTCTCTGGACAGGGTGAGGTCATTGTCTCATCTTCGTGGTTTTTCATGAGA 4620  
 4621 GAAGGAGATGATTCCTTCACGGGGGTCGTGGGGTTTTGCCAGCCGCCCGTGCAGGAGTGG 4680  
 4681 GGAAGGGGCTGAAGCCGAAGACCGTTGGGGGCCGTGGTGAGCTCTGCCTTCTCCAGCTGC 4740  
 4741 TAGAGGCTGGTCTTTCTCATCAGGGAGTGAGGGTCTCGCGTTGGAGACAGTGATCCCCAG 4800  
 4801 GGCGGGATCCTTGCCGTGGCCCTCTGAATGGTCTGGGTGATCCCACACTGATGTCATAAC 4860  
 4861 AGGGAAGTGCCCTGGTTTGGGATTTGTATGCTCACCCAAAGCAAGGGCCTGCTTCCCATC 4920  
 4921 CATTTTGGGAAGGATTTTTTCTCCAGGGGGAGGGTGAAAGCTCTGGGAGGTCTGTGGGCT 4980  
 4981 TACGAGATGGTCCAAGTCCTGGGTCAGTGAGTCCCGGACTCGTGACCGCCTCGAGGAGC 5040  
 5041 CCCCTTCTCCCTACAGGTCATGTTCAATAGGTCAAACAAGGAGGCATGGGTTTCCACCAT 5100  
 5101 CCTGCCGCTGTGATGCAGCCATCGCACTACAGGAGGTAGATCTGTCCAAGGAAATTTGAA 5160  
 5161 TCTCAAGCAATCACTTTCAAGACTGAGCATCTATTGTGCTCAGCCCCAACTGGTGCTATG 5220  
 5221 GGCTCAGAGAAGCTCATCAAATAAATATTAAATCCAGTCTGCCTTCAGGACCTTGCAT 5280  
 5281 TCCAGATGATAACACCTCCCCACACCCCGTCTGCAGAGGCTGTCATTTACCATGGCAA 5340  
 5341 CCGAGCAGCTGAAACACAGTGCGGTCCTCAGCAGGTGGAAAGGCTGAGCTGAGGAGGGCA 5400  
 5401 GTGCCCCGGGCCACAGGCTAACCCTGCTTGCACTTGGTAGCATTTTTACTGTTGGGGCG 5460  
 5461 CATCAGCATCTATTACTGAGAAGCCGCATCCCTTTGAAGCAGGATAGCTGAGACTATAAA 5520  
 5521 AATAAGAAAATACCAGAGTTCCTTGTGGCACAGAGGGCTAAGGATCCAGTGTGTTGCT 5580  
 5581 GCAGCAGCTTGGGTACGGCTGTGGCAAGGGTTCGATCCCTGGCCTGGGAACCTTTCACAT 5640

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[illegible]

**090326Z JUL 78**

# FIG. 2

Size 501 , Select 1

1 ATGCGCTGTGGACCCCTGTGCCGATTCCTGCTGGCTTTGGCCTATCTGTCCTACGTTGAA 60

1 M R C G P L C R F L L A L A Y L S Y V E 20

61 GCCGTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACC 120

21 A V P I W R V Q D D T K T L I K T I V T 40

121 AGGATCAGTGACATTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTG 180

41 R I S D I S H M Q S V S S K Q R V T G L 60

181 GACTTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCG 240

61 D F I P G L H P V L S L S K M D Q T L A 80

241 ATCTACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGAC 300

81 I Y Q Q I L T S L P S R N V I Q I S N D 100

301 CTGGAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCTTGCCC 360

101 L E N L R D L L H L L A S S K S C P L P 120

361 AGCAGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCTGGAAGCCTCCCTCTACTCC 420

121 S R A L E T L E S L G G V L E A S L Y S 140

421 ACGGAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCAGCTG 480

141 T E V V A L S R L Q G A L Q D M L R Q L 160

481 GACCTCAGCCCTGGCTGCTGA 501

161 D L S P G C \* 167

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FIG. 3

1	GTGCCCATCTGGAGAGTCCAGGATGACACCAAAACCCTCATCAAGACGATTGTCACCAGG	60
1	V P I W R V Q D D T K T L I K T I V T R	20
61	ATCAGTGACATTTACACATGCAGTCTGTCTCCTCCAAACAGAGGGTCACCGGTTTGGAC	120
21	I S D I S H M Q S V S S K Q R V T G L D	40
121	TTCATCCCTGGGCTCCATCCTGTCCTGAGTTTGTCCAAGATGGACCAGACCCTGGCGATC	180
41	F I P G L H P V L S L S K M D Q T L A I	60
181	TACCAACAGATCCTCACCAGTCTGCCTTCCAGAAATGTGATCCAAATATCGAATGACCTG	240
61	Y Q Q I L T S L P S R N V I Q I S N D L	80
241	GAGAACCTCCGGGACCTTCTCCACCTGCTGGCCTCCTCCAAGAGCTGCCCCCTTGCCCAGC	300
81	E N L R D L L H L L A S S K S C P L P S	100
301	AGGGCCCTGGAGACCTTGGAGAGCCTGGGCGGCGTCCTGGAAGCCTCCCTCTACTCCACG	360
101	R A L E T L E S L G G V L E A S L Y S T	120
361	GAGGTGGTGGCCCTGAGCAGGCTGCAGGGGGCTCTGCAGGACATGCTGCGGCACGTGGAC	420
121	E V V A L S R L Q G A L Q D M L R H V D	140
421	CTCAGCCCTGGCTGC	435
141	L S P G C	145

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FIG. 4

		10	20	30	40	50	
PIG	1	ATGCGCTGTG	GACCCCTGTG	CCGATTCCCTG	CTGGCTTTGG	GC-TATCTGT	50
HUMAN	1	ATGCATTTGG	GAACCCCTGTG	CGGATTCTTG	-TGGCTTTGG	CCCTATCTTT	50
MOUSE	1	ATGTGCTGGA	GACCCCTGTG	TCCGTTTCCTG	-TGGCTTTGG	TCCTATCTGT	50
		60	70	80	90	100	
PIG	51	CCTACGTTGA	AGCCGTGCCC	ATCTGGGAG	TCCAGGATGA	CACCAAAACC	100
HUMAN	51	TCTATGTCGA	AGCTGTGCCC	ATCCAAAAG	TCCAAGATGA	CACCAAAACC	100
MOUSE	51	CTTATGTTCA	AGCAGTGCCCT	ATCCAGAAAG	TCCAGGATGA	CACCAAAACC	100
		110	120	130	140	150	
PIG	101	CTCATCAAGA	CGATTGTCAC	CAGGATCAAT	GACATTTTAC	ACATGCAGTC	150
HUMAN	101	CTCATCAAGA	CAATTGTCAC	CAGGATCAAT	GACATTTTAC	ACACGCAGTC	150
MOUSE	101	CTCATCAAGA	CGATTGTCAC	CAGGATCAAT	GACATTTTAC	ACACGCAGTC	150
		160	170	180	190	200	
PIG	151	TGTCTCCTCC	AAACAGAGGG	TCACCGGTTT	GGACTTCATC	CCTGGGGCTCC	200
HUMAN	151	AGTCTCCTCC	AAACAGAAAG	TCACCGGTTT	GGACTTCATT	CCTGGGGCTCC	200
MOUSE	151	GCTATCCGCC	AAACAGAGGG	TCACGGGCTT	GGACTTCATT	CCTGGGGCTTC	200
		210	220	230	240	250	
PIG	201	ATCCGTGTCCT	GAGTTTGTCC	AAGATGGACC	AGACCTGGCC	GATCTACCAA	250
HUMAN	201	ACCCCATCCCT	GA CCTTATCC	AAGATGGACC	AGACACTGGC	AGTCTACCAA	250
MOUSE	201	ACCCCATCTCT	GAGTTTGTCC	AAGATGGACC	AGACTCTGGC	AGTCTATCAA	250
		260	270	280	290	300	
PIG	251	CAGATCCCTCA	CCAGTCTGCC	TTCCAGAAAT	GTGATCCAA	TATCGAATGA	300
HUMAN	251	CAGATCCCTCA	CCAGTATGCC	TTCCAGAAAC	GTGATCCAA	TATCCAACTGA	300
MOUSE	251	CAGGTCCCTCA	CCAGCTTGCC	TTCCCAAAAT	GTGCTCCAGA	TACCCAATGA	300
		310	320	330	340	350	
PIG	301	CCTGGAGAAG	CTCCGGGACC	TTCTCCACCT	GCTGGCCTTC	TCCAAGAGCT	350
HUMAN	301	CCTGGAGAAG	CTCCGGGATC	TTCTTCACGT	GCTGGCCTTC	TCTAAGAGCT	350
MOUSE	301	CCTGGAGAAAT	CTCCGAGACC	TCCTCCAICT	GCTGGCCTTC	TCCAAGAGCT	350
		360	370	380	390	400	
PIG	351	GCCCCCTTGGC	CAG---CAGG	GCCTGGAGA	CCTTGGAGAG	CCTGGGCGGC	400
HUMAN	351	GCCACTTGGC	CTGGGCCAGT	GGCCTGGAGA	CCTTGGACAG	CCTGGGCGGT	400
MOUSE	351	GCTCCCTGGC	TCAGACCAGT	GGCCTGCAGA	AGCCAGAGAG	CCTGGATGGC	400
		410	420	430	440	450	
PIG	401	GTCTTGAAG	CCTGCTCTTA	CTCCACGAG	GTGGTGGCCC	TGAGCAGGCT	450
HUMAN	401	GTCTTGAAG	CTTCAAGCTA	CTCCACAGAG	GTGGTGGCCC	TGAGCAGGCT	450
MOUSE	401	GTCTTGAAG	CCTCACTCTA	CTCCACAGAG	GTGGTGGCTT	TGAGCAGGCT	450
		460	470	480	490	500	
PIG	451	GCAGGGGGCT	CTGCAGGACA	TGCTGCGGCA	GCTGGACCTC	AGCCCTGGCT	500
HUMAN	451	GCAGGGGTCT	CTGCAGGACA	TGCTGTGGCA	GCTGGACCTC	AGCCCTGGCT	500
MOUSE	451	GCAGGGCTCT	CTGCAGGACA	TTCTTCAACA	GTGGATGTTT	AGCCCTGAAT	500
		510	520	530	540	550	
PIG	501	GCTGA.....	.....	.....	.....	.....	550
HUMAN	501	GCTGA.....	.....	.....	.....	.....	550
MOUSE	501	GCTGA.....	.....	.....	.....	.....	550

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FOO280" 8882E660

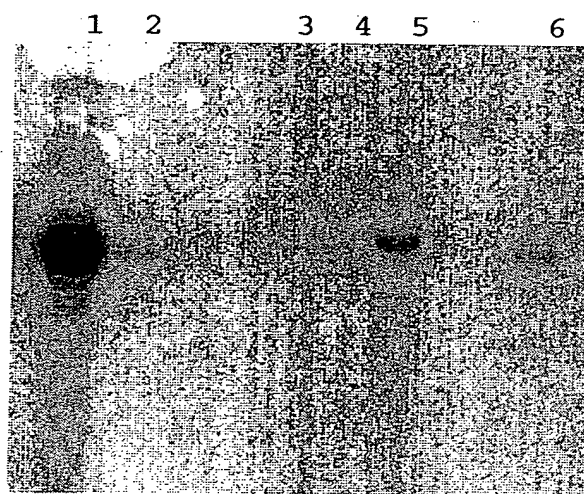


FIG. 5



000280"BBB2E660

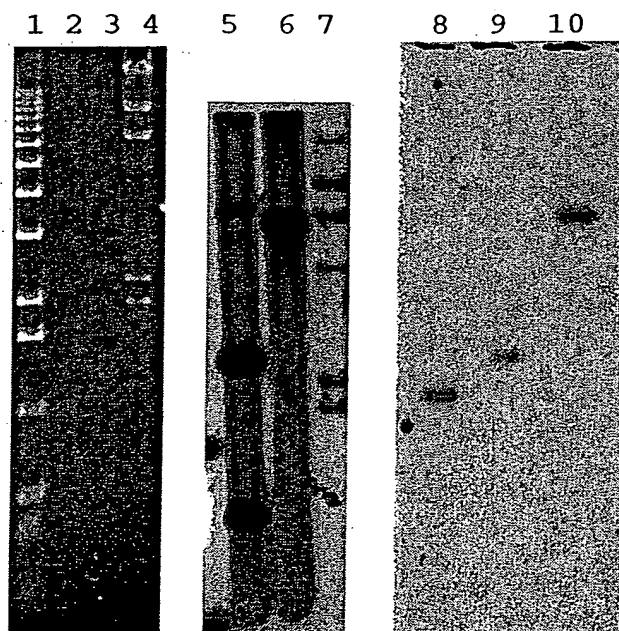


FIG. 6

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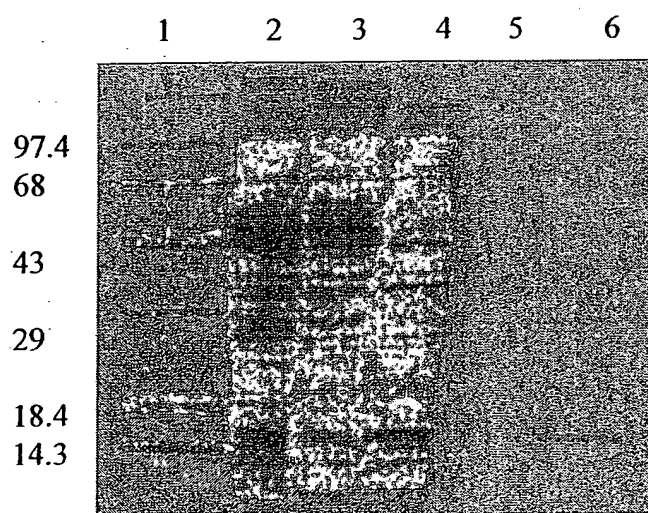


FIG. 7

FIG. 8

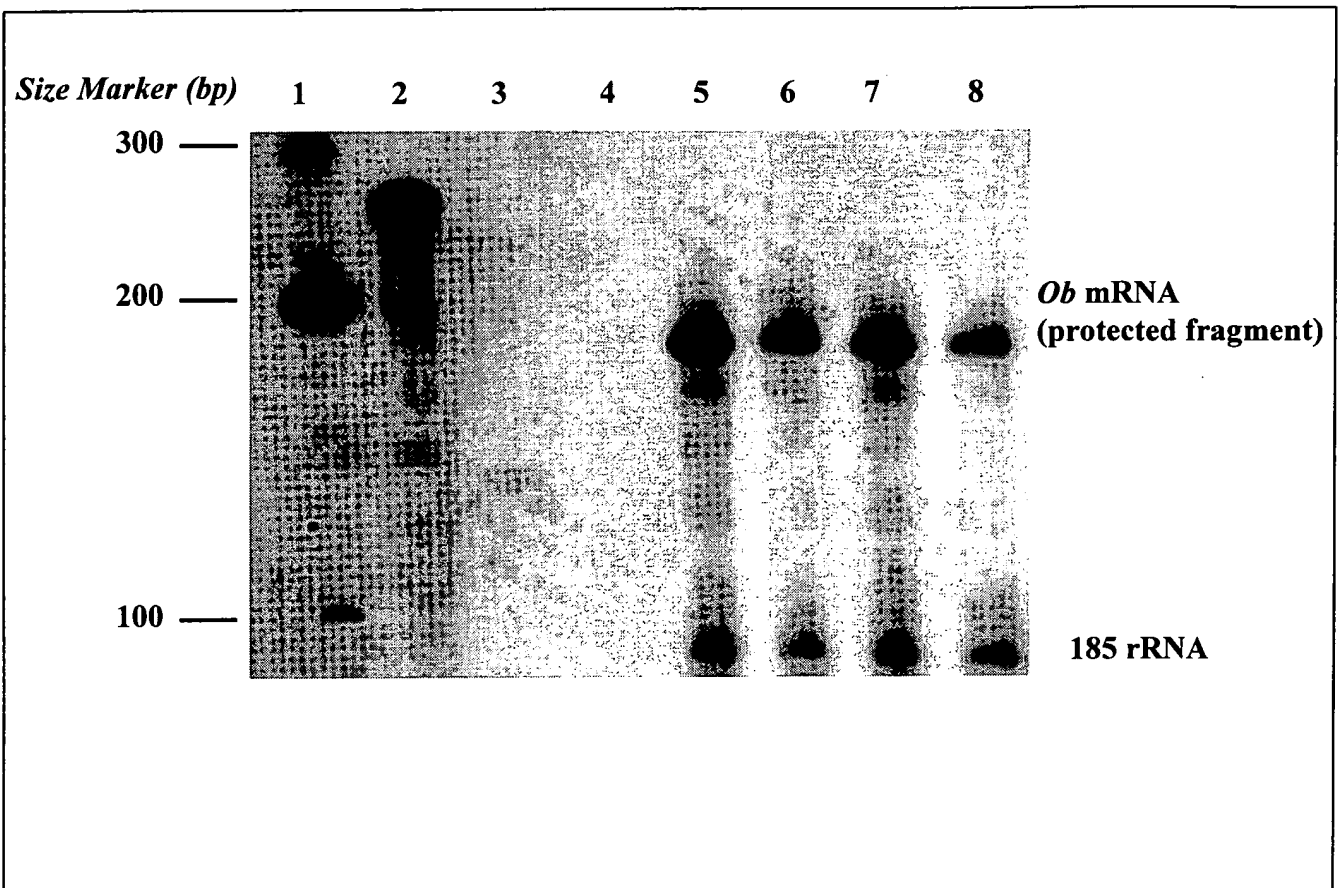


FIG. 9

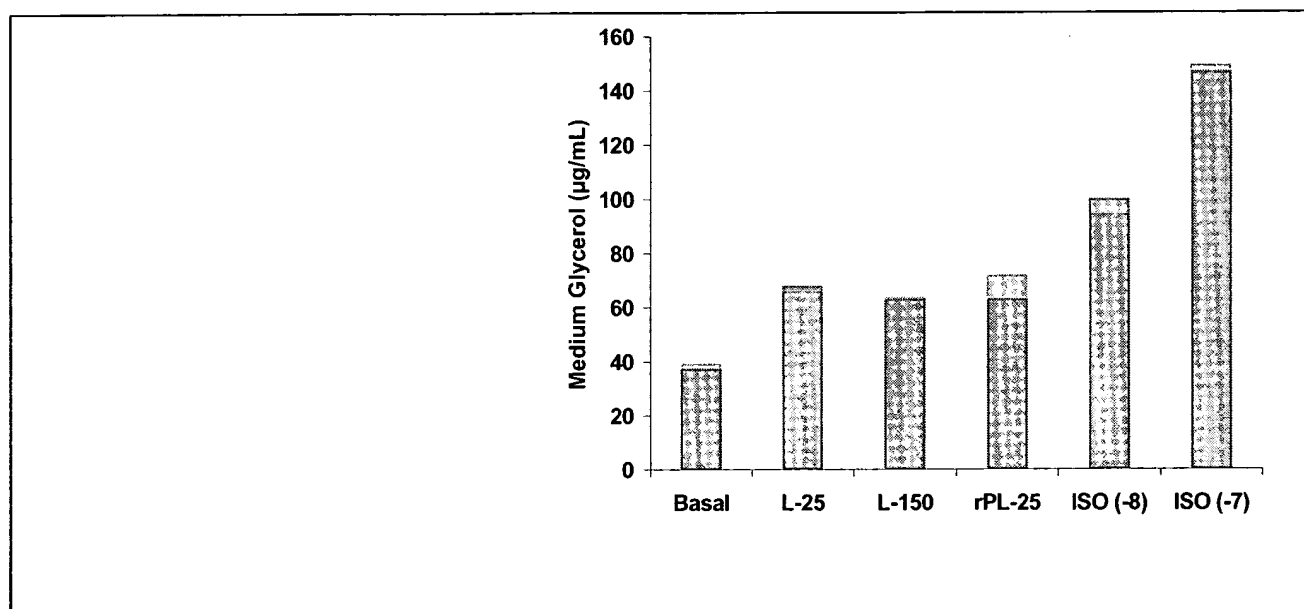
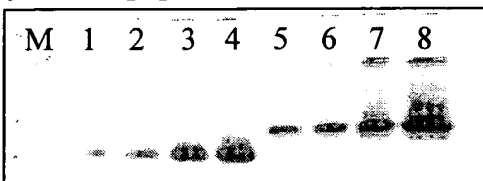


FIG. 10

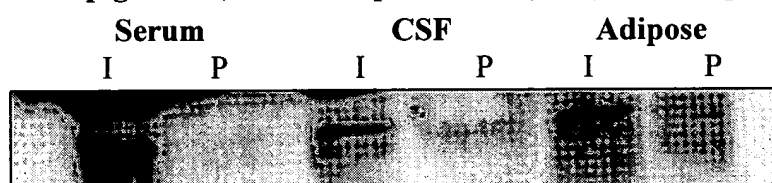
Western blot of recombinant human and porcine leptin with the polyclonal antibody to synthetic peptide based on the C-terminal sequence of porcine leptin.



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FIG. 11

A polyclonal antibody to recombinant porcine leptin immunoprecipitates leptin from pig serum, cerebral spinal fluid (CSF), and adipose extracts.



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